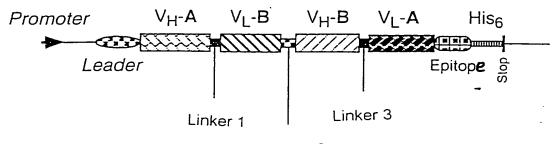
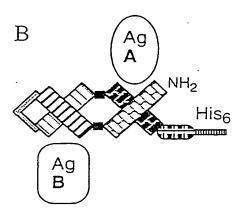
1/10

A



Linker 2



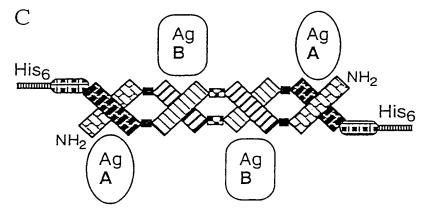
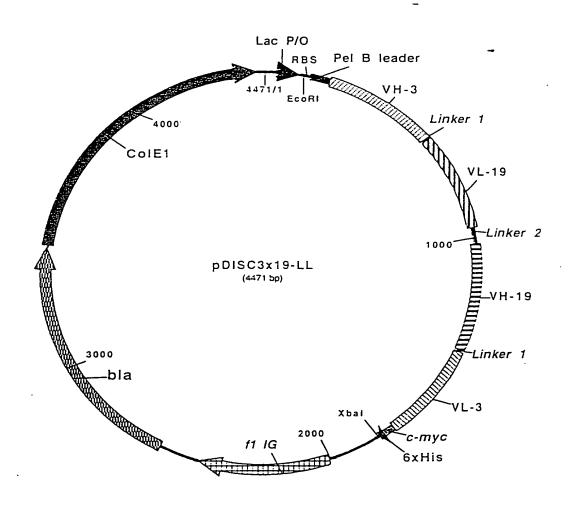


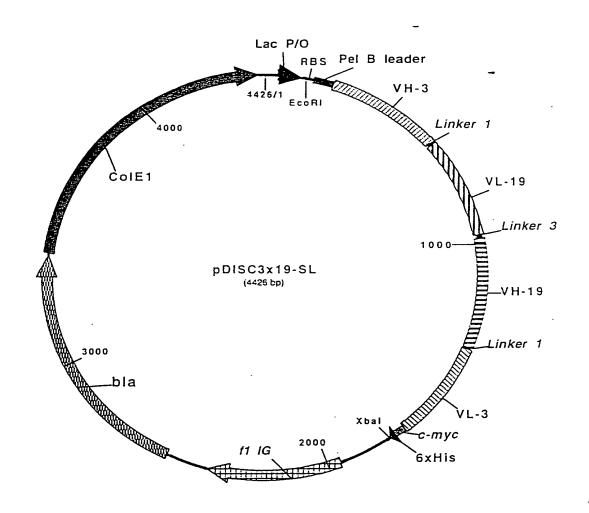
FIGURE 1

Linkers: L1 = GG

 $L2 = (G_4S)_4$ 

L3 = GGPGS





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EcoRI RBS PelB leader Ncol
1 GAATTCATTAAAGAGGAGAAATTAACCA TGAAATACCTATTGCCTACGGCAGCCGCTGGCTGCTGCTGCTGCCAGCAGCCGGCCATCG
D M K Y L E P T A A A G L E E E A A Q P A M
Frame-H1 VH anti-CD3
92 CGCAGGTGCAACTGCAGCAGTCTGGGGCAACTGGGCAACACCTGGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTAC
22 A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T CDR-H1 Frame-H2 CDR-H2
183 TAGGTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCCGTGGTTATAC
52) RYTMHWVKQRPGQGLEWIGYINPSRGYT Frame-H3
267 TAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGCCACAGCCTACATGCAACTGAGCAGCCTGAC
30 N Y N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T CDR-H3
354 ATCTGAGGACTCTGCAGTCTATTACTGTGCAAGATATTATGATGATGATTACAGGCCTTGACTACTGGGGCCAAGGCACCACTCTCA
109 SEDSAVYYCARYYDDHYSLDYWGQGTTL
CH1 Linker 1 Frame-L1 VL anti-CD19
440 CAGTOTOCTCAGCCAAACACACCCCAAGGTTGGGGGGTGATATCTTGGCTCACCCAAACTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGA 138 T V S S A K T T F K L G G D I L L T Q T P A S L A V 5 L G O
CDR-Li
530 GGGCCACCATCTCCTGCAAGGCCAGCAAAGTGTTGATTATGATGGTGATAGTTATTTGAACTGGTACAACACACAC
168 RATISCKASQSVDYDGDSYLNWYQQIPG CDR-L2 Frame-L3
614 AGCCACCCAAACTCCTCATCTATGATGCATCCAAATCTAGTTTTAGTCTAGGATCTCCCACCTTTTAGTCGCAGTCTCCGCACACCTT
196 Q P P K L L I Y D A S N L V S G I P P R F S G S G S G T D F COR-L3 Frame-L4
702 CACCOTCAACATCCATCCTGTGGAGAAGGTGGATGCTGCAACCTATCACTGT <u>CAGCAAAAGTACTGAGGAT</u> CCGTGGACGTTCGGTGGA
225 TLNIHPVEKVDAATYHCQQSTEDPWTFGG
C kacca Notl Linker 2
790 GGCACCAAGCTGGAAATCAAA <u>CGGGCTGATGCT</u> GCGGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG
255 G T K L E I K R A D A A A A G G G G S G G G G G G
Byull Srama-H1 VH anti CD19
Pvull Frame-H1 VH anti-CD19 874 TCCGGTGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGCAGCCTGGGCCTGGGTCGTCAGTGAAGATTTCCTGCAAGG
874 TCCGGTGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGGGGCTGGGTCGTCAGTGAGAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K
874 TCCGGTGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGGGGCTGGTGCAGGGGTCGTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2
874 TCCGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGAATGAACTGGGTGAAGCAGGGCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC
874 TCCGGTGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGGGGCTGGTGCAGGGGTCGTCAGTGAAGATTTCCTGCAAGG 283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2
874 TCCGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCTGGGGCTGGGTCAGGGCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGAGATTTGGC 312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W PStl Frame-H3 1049 CTGGAGATGGTGATACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGACCAATCCTCCAGCACAGCCTACA
874 TCCGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCGGGGCTGAGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGGGCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W PStl Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACGACGACGAATCCTCCAGCACAACCCTACA 341 P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y
874 TCCGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGCTGGGGCTGAGCCTGGGTCCTCAGTGAAGATTMCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAACTGGGTGAACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStl Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACACCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3
874 TCCGGTGGTGGTAGCCAGGTGCAGCTGCAGCAGTCGGGGCTGAGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGGGCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W PStl Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACGACGACGAATCCTCCAGCACAACCCTACA 341 P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y
874 TCCGGTGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGCTGGGGCTGGGTCCTCAGTGAAGATTMCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAACTGGGAAGCCCTGGACAGGGTCTTGAGTGGATTGGACAGAGTTTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PStl Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGCACAATCCTCCAGCACAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y  CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTCAGGACTCTGCGGTCTATTTCTGTGCAACACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y  Frame-H4 CH1 Linker 1 Frame-L1
874 TCCGGTGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGCTGGGCTGAGCCTGGGTCCTCAGTGAAGATTMCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2 CDR-H2 962 CTMCTGGCTATGCATTCAGTAGCTAGTGGATGGAACTGGGTGAAGCAGAGGCCTTGGACAGGGTCTTGAGTGGACAGAGTTTGGACAGAGTTTTGGACAGAGTATTTTGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PStl Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACACAAATCCTCCAGCCTACA 341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAACCCCCAGCCTCACCCCCAAGCTTGGGGGGTGATATCGTGCTCACCCC
874 TCCGGTGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGCTGGGGCTGGTCCAGCAGCTGGTCAAGAGTTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGGATGGAACTGGGTGAAGCAGAGGCGTGTGAGCAGGGTCTTGAGTGGACAGAGTGGACAGAGAGTTGGACAGAGAGTTGGACAGAGAGAG
874 TCCGGTGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGCTGGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG 283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1 Frame-H2 CDR-H2  962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCAGCGCTTGACCAGCGTCTTGAGTGGACAGACTATGGC 312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PStl Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTTGACTGCAGACCAATCCTCAGCACAATCCTCAGCACAATCCTCAGCACAATCCTCAGCACAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAATCCTCAGCACCAACCTTAGCAACTAACAACTAACAACTAACT
874 TCCGGTGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGCTGGGCCTGAGCTGGTCCTCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1 Frame-H2 CDR-H2  962 CTTCTGCCTATGCATTCAGTAGCTAGCTGGATGAACTGGGTGAAGCACGCCTGGACAGGGTCTTGAGTGGACAGAGTTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PStI Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACGACGAATCCTCCAGCACAGACTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y  CDR-H3  1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTTGCGGTCTATTTCTGTGCAAGACGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y  Frame-H4 CHI Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGACACCTCAGCCGAAGCTTGGGGGTGATATCGTCCACCTC 398) A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T  VL anti-CD3  CDR-L1 1307 AGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACGTGAAGTGTAAGTTACATGAACTGG
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874 TCCGGTGGTGGTAGCLAGGTGCAGCTGCAGCAGTCTGGGCTGTGAGCCTGGTCCTCAGTGAAGATTACTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X COR-H1 Frame-H2 CDR-H2 962 CTTCTGGCTATGCATTCAGTAGCTAGTGAACTGGGTGAAGCAGAGGGTCTTGAGTGGATTGAGCAGAGTTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PSII Frame-H3 1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCAACTCTGACTGCAGACGAATCCTCAGCACAGCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y CDR-H3 1133 TGCAACTCAGCAGCCTTAGCATCTGAGGACTCTGCGGTCTAGTTCTGGCAGGAGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Frame-H4 CH1 Linker 1 Frame-L1 1219 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGGCTAAAACAACCCCAAGCTTGGCGGTGATATCGTGCTCACTC 398) A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T VL anti-CD3 CDR-L1 1307 AGTCTCAGCAATCATGTCTGCATCTCCAGCGAAGCTCAGCTGCAGGTGAAGCTAGAACTGGGGTAAGTTACATGAACTGG 427) Q S P A I M S A S P G E X V T M T C S A S S S V S Y M N W Frame-L2 CDR-L2 Frame-L3 1393 TACCAGCAGAAGTCAGGCACCTCCCCCAAAAAGGATGGCTTCACTCCAGCTAAAACTGGGCTTCTCAGCGGGAA
### ##################################
### ##################################
874 TCCGGTGGTGGTGGTAGCCAGTGCAGCTGCAGCAGTCTGGGCCTGAGCCTGGTCCAGTGAAGATTTCCTGCAAGG 283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X CDR-H1 Frame-H2  962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAAGCCAGCGTCTTGAGTGGATTGGACAGGATTTGGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W PSII Frame-H3  1049 CTGGGGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTTGACTGCAGACCAACCA
### ##################################
874 TCCGGTGGTGGTGGTAGCCAGCTGCAGCTGCAGCTGCAGCTGGTCTCAGCTCTCAGTGAAGATTTCCTCCAAGG 283) S G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1  Frame-H2  62 CTTCTGGCTATGCATTCAGTAGCTACCTGGATGAACTGGGTGGATGGA
### ##################################
874 TCCGGTGGTGGTGGTAGCNGGTCCACCTGAGCAGCTCTGCGCTCAGCTCA
874 TCCGGTGGTGGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA

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EcoRI RBS PelB leader Ncol
E GAATTCATTAAA <u>GAGGAG</u> AAATTAACCATGAAATACCTATTGCCTACGGCAGCCGCTGCCTGC
1 M X Y L L P T A A A G L L L A A Q P A M
Frame-H1 VH anti-CD3 92 CGCAGGTGCAACTGCAGCAGTCTGGGGCTGAACTGGCGAACTGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTAC
22) A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T
CDR-H1 Frame-H2 CDR-H2 →
183 TAGGTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATTACATTAATCCTAGCCGTGGTTATAC
52) RYTMHWVKQRPGQGLEWIGYINPSRG <del>yT</del>
Frame-H3
267 TAATTACAATCAGAAGTTCAAGGACAAGGCCACATTGACTACAGAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGAC 80 N Y N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T
CDR-H3 Frame-H4 354 ATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u> TGGGGCCAAGGCACCACTCTCA
109) S E D S A V Y Y C A R Y Y D D H Y S L D Y W G Q G F F L
CH1 Linker 1 Frame-Li VL anti-CD19
440 CAGTCTCCTCAGCCAAAACAACACCCAACCTTGGCGGTGATATCTTGCTCAACCCAAACTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGA
138 T V S S A K T T P K L G G D I L L T Q T P A S L A V S L 3 Q
CDR-L1 Frame-L2
530 GGGCCATCTGCAAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTGAACTGGTACAACAACTAGTACCAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTACAACAACTAGTAACTAGTAAACTAGTAAACTAGTAACTAAC
168 RATISCKASQSVDYDGDSYENWYQQIFG
CDR-L2 Frame-L3
514 AGCCACCCAAACTCCTCATCTATGATGCATCCAATCTAGTTTCTGGGATCCCACCCA
196 Q P P K L L I Y D A S N L V S G I P P R F S G S G S G T D F
CDR-L3 Frame-L4
702 CACCCTCAACATCCATCCTGTGGAGAAGGTGGATGCTGCAACCTATCACTGT <u>CAGCAAAAGTACTGAGGAT</u> CCGTGGACGTTCGGTGGA
225 TENIH PVEKVDAATYHOQQSTEDPWTFGG
Ckappa Notl Linker 3 Pvull Frame-H1
790 GGCACCAAGCTGGAAATCAAA <u>CGCCCTCATGCT</u> GCGGCCCCTGGTGGCCCAGGGTCGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCT
255 G T K L E I K R A D A A A G G P G S Q V Q L Q Q S G A E L
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19 CDR-H1 Frame-H2
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1 Frame-H2  879 GGTGAGGCCTGGGTGAGGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  679 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAAGCAGGCC  284 V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTGAGGATTTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCCTCAGTGAACATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGAAGTGAACTGGGTGAAGCAGAGGC  284 V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTGGAGTGGATTTGGACAGATTTGGCCTGGAGATGATGAATTGAAAGTTCAAGGGTAAAGCC
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAAGTGAAGTGAAGTGAAGCAGGCC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGGACTTGGACTTTGGCCTGGAGATGAAGTACAATGGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCATGAACATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTTGGGTAAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGGACTGGATTTGGACAGATTTGGCCTGGAGATGTGAACTAACT
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGGATGAACTGGGTGAAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTTGGCCTGGAGATGGTGATACTAACTA
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGGATGAACTGGGTGAAGCAGGCC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGGTGAAGCTAAAGTACAATGGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A Frame-H3  1051 ACTCTGACTGCAGAGAATCCTCCAGCACAGCCTACATCCAACTCAGCAGCTTAGGACTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAAGCAGAGCC 284) V R P G S S V X I S C X A S G Y A F S S Y W M N W V X Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTTGGCCTGGAGATGGTGATACTAACTA
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGATGAAGCAGGCC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTTGGACAGATTTTGGCCTGGAGAGTGAACTAACT
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  379 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  379 GGTCAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTACTGGAAGATGAACTGGGTAAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTTGGCTGGGATGATACTAACAATGGAAAGTTCAAGGGTAAAGCC  314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCCAGCCTACATCCAACTCAGCAGCCTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAC  342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  Frame-H4  CH1  1142 GGGAGACTACGAGGGTAGGCCGTTATTACTATGCTATGGACTTACGGAACCTCAGGCACTCCCAGCCCTACCTCCCCAGCCAAAC  372) R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K  Linker 1 Frame-L1 VL anti-CD3  1226 CAACACCCAAGCTTGGGGGTGATATCGTGCTCACCTACCT
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
VH anti-CD19  CDR-H1  Frame-H2  879 GGTCAGGCCTCGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGC
VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGCCTGGGTCCTCAGTGAACATTTCCTGCAACGCTTCTGCTATGCATTCAGTAGCTGAACATTCAGTGAACATTCCTGCAACGCTTCTGCTATGCATTCAGTAGCTTCAGTGAACATTCAGTGAACATTCAGTAGCTTCAGTGAACATTCAGTAGCTGAACATTCAGTAGCTGAACATTCAGTAGCTGAACATTCAGTAGCTGAACATTCAGTAGCTGAACATTCAGTAGCTGAACATTCAGTGAACATTCAGTGAACATTCAGTGAACATTCAGTGAACATTCAGTGAACATTCAAGTGAAAGATTCAAGGGTAAAGCC  314 P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGCGAACCTACCACCCTACATCCAACTCAGCAGCCTAGCATCTGAGGACCTCTGCGGTCTATTTCTGTGCAAGAC  342 T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  Frame-H4  CH1  1142 GGGAGACTACGAGGGTAGGCCGTTATTACTATGCTATGGACTACTGCAGCAACCTCAGGCAACCTCAGTCACCGTCTCCTCAGCTAAAA  372 R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K  Linker 1 Frame-L1 VL anti-CD3  1226 CAACACCCAACCTTGGGGGTGATATTCGGGTCTCAGGCAACCTCAGCCAACCACCTAGCACCTAGCACCTAGCACCTAGCACCTAGCACCTACCACCTAGCACCTAGCACCTAGCACCTAGCACCTACCCTCCAGCCAACCATTGGACCTCCAGGCGAACCTCAGCCACCAACCA
VH anti-CD19  CDR-H1  Frame-H2  879 GGTCAGGCCTCGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGC
VH anti-CD19  STATE OF TEXT OF THE TEXT OF
VH anti-CD19  VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGGCCTGGGGTGAAGATTTCGCAAGGCTTCTGGCTATGCATTCAGTAGGAAGATGGAAAGTTCAAGGGGC 284) V R P G S S V X I S C K A S G Y A F S S Y W M N W V X Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGAATTTGGCTATGGCTTGGCT
VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCAGGAGATTTCCTGCAAGGCTTCTGCCTATGCATGC
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  Frame-H2  379 GGTGAGGCTGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGCTATGCATTCATT
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L

941 ATGAGATTTCCTTCAATTTTTACTGCTGTTTTATTCGCAGCATCCTCCGCATTAGCTGCTCCAGTCAACACTAC 1 M R F P S I F T A V L F A A S S A L A A P V N T T alpha-factor signal 1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG 25) TEDETAQIPAEAVIGYSDLEGDF.D 1089 TTGCTGTTTTGCCATTTTCCAACAGCACAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT 50 V A V L P F S N S T N N G L L F I N T T I A S I A m EcoRi الية: Xhol 1163 CCTALAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGCTGAAGCT<u>GAATTC</u>CAGGTGCAACTGCAGCAGTC 75 A K E E G V S L E K R E A E A E F Q V Q L Q Q S VH anti-CD3 1 1234 TGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT 98 G A E L A R P G A S V K M S C K A S IД Ш į

FIGURE 7

941 ATGAGATTTCCTTCAATTTTTACTGCTGTTTTATTCGCAGCATCCTCCGCATTAGCTGCTCCAGTCAACACTAC 1 M R F P S I F T A V L F A A S S A L A A P V N T T alpha-factor signal 1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG 25) TEDETAQI-PAEAVIGYSDLEGDFD 1089 TTGCTGTTTTGCCATTTTCCAACAGCACAAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT 50 V A V L P F S N S T N N G L L F I N T T I A S I A ,Ã **EcoRI** Xhol 1163 GCTAAAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGGCTGAAGCT<u>GAATTC</u>ATGGCGCAGGTGCAACTGCAG 75 A K E E G V S L E K R E A E A E F M A Q V Q L Q VH anti-CD3 1235 CAGTCTGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT 99 Q S G A E L A R P G A S V K M S C K A S ij IJ O 4

FIGURE 8

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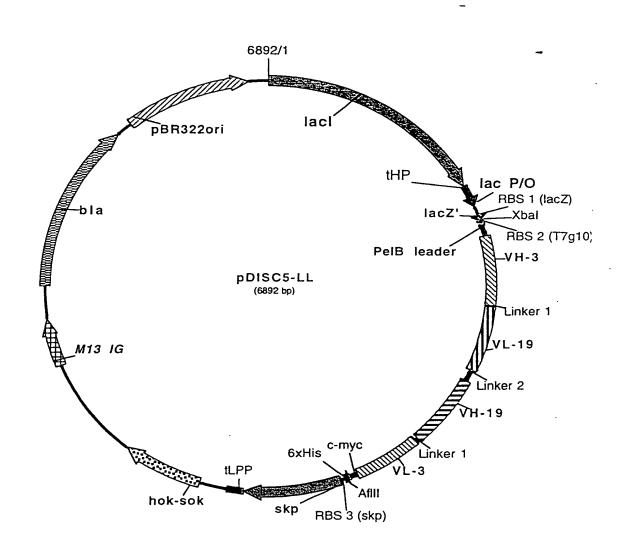


FIGURE 9

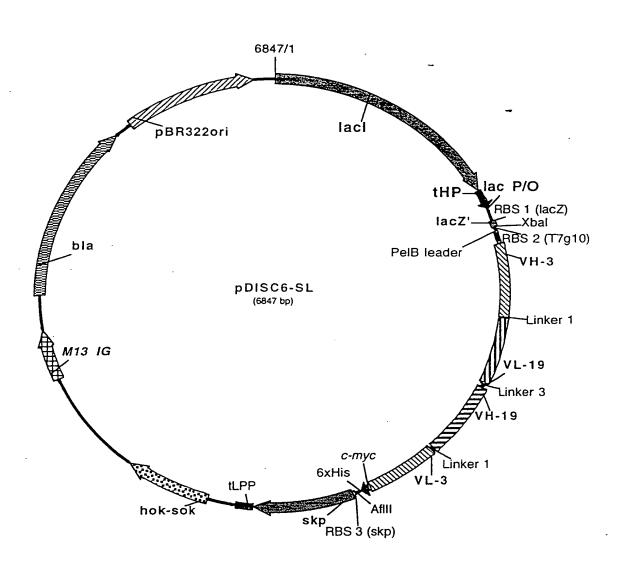


FIGURE 10